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09/865,090	05/24/2001	Harold R. Garner	UTSD:0668	2902

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RICHARD ARON OSMAN
SCIENCE AND TECHNOLOGY LAW GROUP
75 DENISE DRIVE
HILLSBOROUGH, CA 94010

EXAMINER	
WONG, LESLIE	
ART UNIT	**PAPER NUMBER**
2177	

DATE MAILED: 10/31/2003

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/865,090	GARNER ET AL.	
	Examiner	Art Unit	
	Leslie Wong	2177	

-- *The MAILING DATE of this communication appears on the cover sheet with the correspondence address* --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *24 May 2001*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-24* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-24* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11)☐ The proposed drawing correction filed on _____ is: a)☐ approved b)☐ disapproved by the Examiner.

If approved, corrected drawings are required in reply to this Office action.

12)☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

13)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

14)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).

a) ☐ The translation of the foreign language provisional application has been received.

15)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449) Paper No(s) _____.
4) ☐ Interview Summary (PTO-413) Paper No(s). _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other:

DETAILED ACTION

Specification

1. The title of the invention is not descriptive. A new title is required that is clearly indicative of the invention to which the claims are directed.

2. The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code. Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. See MPEP § 608.01. Alternatively, Applicants can place the URL between angle brackets (i.e., <>).

Claim Rejections - 35 USC § 102

3. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

4. Claims 1-4, 6, 8-24 are rejected under 35 U.S.C. 102(e) as being anticipated by **Ford et al.** (U.S. Patent 6,472,173 B1).

Regarding claims 1, 13, and 17, **Ford et al.** teach computer-based system for creating a targeted collection of sequences from a dataset comprising sequence

identifiers corresponding to natural complex biopolymer sequences and linked to corresponding annotations, the system comprising:

a). a search function which searches the annotations of the dataset (i.e., fragments or regions of a know sequence) according to a user defined criterion (i.e., target sequence or target structural motif) and outputs a first subset of the dataset restricted by the criterion (col. 23, lines 46-52; col. 23, line 64 – col. 24, line 17);

b). a redundancy reducing function which compares the first subset with a first database correlating the sequence identifiers (EMFs sequences can be identified within an "intergenic segment" refers to the fragments of a genome) of the first subset with syngeneic biopolymers and outputs a second subset of the dataset having reduced unique, natural complex biopolymer redundancy relative to the first subset (col. 24, lines 20-30);

c). a selection function which applies to the second subset a user-defined selection parameter (EMF trap vector) and outputs a third subset (i.e., identifiable phonotypes as output of a third subset which are identified when the EMF trap vector is placed within a appropriate host under appropriate conditions) restricted relative to the second subset by the parameter (col. 24, lines 31-41); and

d). a tabulation function which creates and outputs the targeted collection of sequences in the form of a data table comprising, configurable by and sortable by the sequence identifiers of the third subset (col. 27, line 65 – col. 29, line 50).

Regarding claim 2, **Ford et al**. further teach wherein the criterion is selected from the group consisting of a keyword and a concept (i.e., target sequence, target structure motif) (col. 34, line 64 – col. 24, line 17).

Regarding claim 3, **Ford et al**. further teach wherein the criterion is one of a plurality of user-defined criteria, and the search function searches the annotations of the dataset according to the criteria and outputs a first subset of the dataset restricted by the criteria (col. 23, lines 46-52).

Regarding claim 4, **Ford et al**. further teach wherein the criterion is one of a plurality of user-defined criteria, and the search function searches the annotations of the dataset according to the criteria and outputs a first subset of the dataset restricted by the criteria, wherein the criteria include multiple keywords (col. 24, lines 8-17).

Regarding claim 6, **Ford et al**. further teach wherein the dataset is one of a plurality of datasets (i.e., homology regions), and the search function searches the annotations of the datasets according to the user-defined criterion and outputs a first subset of the datasets restricted by the criterion (col. 28, lines 14-39).

Regarding claim 8, **Ford et al**. further teach wherein the database is one of a plurality of databases correlating the sequence identifiers of the first subset with syngeneic biopolymers, and the redundancy reducing function compares the first subset

with the databases and outputs the second subset of the dataset (col. 23, lines 36-45; col. 28, lines 31-39).

Regarding claims 9 and 16, **Ford et al**. further teach wherein the parameter is selected from the group consisting of source (i.e., Genbank), species (i.e., homology), author (i.e., Applied Biosystems) and pathway (i.e., INHERIT 670) (col. 28, lines 15-39).

Regarding claim 10, **Ford et al**. further teach wherein the parameter is one of a plurality of user-defined selection parameters, and the selection function applies to the second subset the parameters and outputs the third subset restricted relative to the second subset by the parameters (col. 24, lines 31-41).

Regarding claim 11, **Ford et al**. further teach wherein the redundancy reducing function outputs a second subset of the dataset which eliminates unique, natural complex biopolymer redundancy relative to the first subset (col. 24, lines 20-30).

Regarding claim 12, **Ford et al**. further teach comprising an expansion function which searches a second database for synonyms of the sequence identifiers of the first, second or third subset (col. 24, lines 20-30).

Regarding claim 14, **Ford et al**. further teach computer-based system for creating a targeted collection of sequences from a plurality of datasets comprising

sequence identifiers corresponding to natural complex biopolymer sequences, the system comprising:

a). a merge and redundancy reducing function which compares the datasets with a database correlating the sequence identifiers with syngencic biopolymers and creates a subset of the sum of the datasets having reduced unique, natural complex biopolymer redundancy relative to the sum (col. 28, lines 14-51); and

b). a tabulation function which creates and outputs the targeted collection of sequences in the form of a data table comprising, configurable by and sortable by the sequence identifiers of the subset (col. 29, line 17 – col. 30, line 16).

Regarding claim 15, **Ford et al**. further teach wherein the merge and redundancy reducing function further comprises a selection function which applies a user-defined selection parameter whereby the subset is restricted relative to the sum of the datasets by the parameter (col. 24, lines 31-41).

Regarding claim 19, **Ford et al**. further teach wherein the second annotations comprise data attributable to and correlated with at least a subset of the sequence identifiers or sequences of the dataset, said data selected from the group consisting of: gene expression data, sequencing data, genotype data, polymorphism data and clinical data (col. 24, lines 33-49).

Regarding claims 18 and 20, **Ford et al**. further teach a computer-based method for creating a targeted collection of sequences from a dataset comprising sequence identifiers corresponding to natural complex biopolymer sequences and linked to corresponding first annotations, the method comprising computer-implemented steps of:

a). merging the dataset with a database comprising second annotations attributable to and correlated with at least a subset of the sequence identifiers or sequences of the dataset and linking the second annotations to the corresponding sequence identifiers of the subset (col. 23, line 64 – col. 24, line 17; col. 23, lines 46-62, col. 24, lines 20-30; col. 29, line 17 – col. 30, line 16); and

b). creating and outputting the targeted collection of sequences in the form of a data table comprising, configurable by and sortable by the sequence identifiers of the subset and the second annotations (col. 27, line 65 – col. 29, line 50).

Regarding claim 21, **Ford et al**. further teach a second computer-based system for creating a targeted collection of sequences from a plurality of datasets comprising sequence identifiers corresponding to natural complex biopolymer sequences, the second system comprising:

a). a merge and redundancy reducing function which compares the datasets with a database correlating the sequence identifiers with syngeneic biopolymers and creates a subset of the sum of the datasets having reduced unique, natural complex biopolymer redundancy relative to the sum (col. 24, lines 20-49); and

b). a tabulation function which creates and outputs the targeted collection of sequences in the form of a data table comprising, configurable by and sortable by the sequence identifiers of the subset (col. 29, lines 17-50).

Regarding claim 22, **Ford et al**. further teach a second computer-based system for creating a targeted collection of sequences from a dataset comprising sequence identifiers corresponding to natural complex biopolymer sequences and linked to corresponding first annotations, the second system comprising:

a). an integration function which merges the dataset with a database comprising second annotations attributable to and correlated with at least a subset of the sequence identifiers or sequences of the dataset and which link.; the second annotations to the corresponding sequence identifiers of the subset (col. 28, lines 14-51); and

b). a tabulation function which creates and outputs the targeted collection of sequences in the form of a data table comprising, configurable by and sortable by the sequence identifiers of the subset and the second annotations (col. 29, line 17 – col. 30, line 16).

Regarding claim 23, **Ford et al**. further teach steps of:

a). a merge and redundancy reducing function which compares the datasets with a database correlating the sequence identifiers with syngeneic biopolymers and

creates a subset of the sum of the datasets having reduced unique, natural complex biopolymer redundancy relative to the sum (col. 28, lines 14-51); and

b). a tabulation function which crates and outputs the targeted collection of sequences in the form of a data table comprising, configurable by and sortable by the sequence identifiers of the subset (col. 29, line 17 – col. 30, line 16); and,

c). a third computer-based system for creating a targeted collection of sequences from a dataset comprising sequence identifiers corresponding to natural complex biopolymer sequences and linked to corresponding first annotations, the third system comprising:

1). an integration function which merges the dataset with a database comprising second annotations attributable to and correlated with at least a subset of the sequence identifiers or sequences of the dataset and which link, the second annotations to the corresponding sequence identifiers of the subset (col. 28, lines 14-51); and

2). a tabulation function which creates and outputs the targeted collection of sequences in the form of a data table comprising, configurable by and sortable by the sequence identifiers of the subset and the second annotations (col. 24, lines 45-49; col. 30, lines 10-17).

Regarding claim 24, **Ford et al**. further teach wherein the system is ARROGANT (col. 81, line 30 - col. 82, line 32; see Example 33). The cited portion facilitates

identification, analysis, and comparison of collections of genes and clones. Therefore, it is equivalent to the ARROGANT system.

Claim Rejections - 35 USC § 103

5. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

6. Claim 5 is rejected under 35 U.S.C. 103(a) as being unpatentable over **Ford et al.** (U.S. Patent 6,472,173 B1) as applied to claims 1-4, 6, 8-24 above, and further in view of **Chin et al.** (U.S. Patent 6,470,277).

Regarding claim 5, **Ford et al**. further teach wherein the dataset is selected from GenBank (col. 28, lines 14-17)

Ford et al. do not explicitly teach wherein the dataset is selected from the group consisting GenBank, Medline, and KEGG.

Chin et al., however, teach wherein the dataset is selected from the group consisting Medline and KEGG (col. 11, lines 29-46; col. 18, lines 54-59).

It would have been obvious to one of ordinary skill in the art at the time of the invention was made to include Medline and KEGG for sequence searching because these databases contain functional information related to known genes and would be helpful for researchers to be able to access the mentioned databases.

7. Claim 7 is rejected under 35 U.S.C. 103(a) as being unpatentable over **Ford et al.** (U.S. Patent 6,472,173 B1) as applied to claims 1-4, 6, 8-24 above, and further in view of **MacLeod et al.** (U.S. Patent 6,221,600 B1).

Regarding claim 7, **Ford et al**. do not explicitly teach wherein the database is selected from the group consisting of UniGene and LocusLink.

MacLeod et al., however, teach wherein the database is selected from the group consisting of UniGene and LocusLink (col. 13, lines 43-58).

It would have been obvious to one of ordinary skill in the art at the time of the invention was made to allow users to have access to UniGene and LocusLink to search

and create collections of sequences as this would provide various of sources for users to search, extract, and manipulate the information.

Conclusion

8. The prior art made of record and not relied upon is considered pertinent to applicant's disclosure.

Bjornson et al. (U.S. 2002/0194173 A1)

Castelli et al. (U.S. Patent 5,940,825)

Hubbell et al. (U.S. Patent 5,571,639)

Au-Young et al. (U.S. Patent 6,500,938)

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Leslie Wong whose telephone number is (703) 305-3018. The examiner can normally be reached on Monday to Friday 9:30am - 6:30 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, John E Breene can be reached on (703) 305-9790. The fax phone number for the organization where this application or proceeding is assigned is (703) 872-9306.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (703) 305-3900.

Leslie Wong
Patent Examiner
Art Unit 2177

Lw
October 19, 2003

JEAN R. HOMERE
PRIMARY EXAMINER